

Figure 1
Nucleotide Sequence and predicted protein for HLTDG74

	10	30	50	
-88	GTTTGCTCTGGGCAGCCAAGTTGGCATATTGGAAGCTTTTCCGGGCTCTGGAGGGT-29			
	70	90	110	
-28	CCCTGCTTCTTCTACAGCCGTTCCGGGCATGGCCTGGCTGGGGCGCTCGCTCCACGTCT			31
-8	M A W L G A S L H V W			11
	130	150	170	
32	GGGGTTGGCTAATGCTCGGCAGCTGCCCTGGCCAGAGCCCAGCTGGATTCTGATGGCA			91
12	G W L M L G S C L L A R A Q L D S D G T			31
	190	210	230	
92	CCATCACTATAGAGGAGCAGATTGTCCTTGTGCTGAAAGCGAAAGTACAATGTGAACCTCA			151
32	I T I E E Q I V L V L K A K V Q C E L N			51
	250	270	290	
152	ACATCACAGCTCAACTCCAGGAGGGAGAAGGTAATTGTTCCCTGAATGGGATGGACTCA			211
52	I T A Q L Q E G E G N C F P E W D G L I			71
	310	330	350	
212	TTTGTGGCCACAGGAAACAGTGGGAAAATATCGGCTGTTCCATGCCCTCTTATATT			271
72	C W P R G T V G K I S A V P C P P Y I Y			91
	370	390	410	
272	ATGACTTCAACCATAAAGGAGTTGCTTCCGACACTGTAACCCCAATGGAACATGGATT			331
92	D F N H K G V A F R H C N P N G T W D F			111
	430	450	470	
332	TTATGCACAGCTTAAATAAACATGGCCAATTATTCACTGTAACCCCAATGGAACATGGCAGC			391
112	M H S L N K T W A N Y S D C L R F L Q P			131
	490	510	530	
392	CAGATATCAGCATAGGAAAGCAAGAATTCTGTGAACGCCCTATGTAATGTATAACCGTTG			451
132	D I - S - I G K Q E F C E R L Y V M Y T V G			151
	550	570	590	
452	GCTACTCCATCTTTGGTCTTGGCTGTGGCTATTCTCATCATTGGTACTTCAGAC			511
152	Y S I S F G S L A V A I L I I G Y F R R			171
	610	630	650	
512	GATTGCATTGCACTAGGAACTATATCCACATGCACTTATTGTGTCTTCATGCTGAGAG			571
172	L H C T R N Y I H M H L F V S F M L R A			191
	670	690	710	
572	CTACAAGCATTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG			631
192	T S I F V K D R V V H A H I G V K E L E			211

FIGURE 1 1/3

	730	750	770	
632	AGTCCCTAATAATGCAGGATGACCCACAAAATTCCATTGAGGCAACTCTGTGGACAAAT			691
212	S L I M Q D D P Q N S I E A T S V D K S			231
	790	810	830	
692	CACAATATATCGGGTGCAAGATTGCTGTTGTGATGTTTATTTACTTCCTGGCTACAAATT			751
232	Q Y I G C K I A V V M F I Y F L A T N Y			251
	850	870	890	
752	ATTATTGGATCCTGGTGGAAAGGTCTCACCTGCATAATCTCATCTTGTGGCTTCTTT			811
252	Y W I L V E G L Y L H N L I F V A F F S			271
	910	930	950	
812	CGGACACCAAATACTGTGGGGCTTCATCTTGATAGGCTGGGGTTCCAGCAGCATTTG			871
272	D T K Y L W G F I L I G W G F P A A F V			291
	970	990	1010	
872	TTGCAGCATGGGCTGTGGCACGAGCAACTCTGGCTGATGGAGGTGCTGGGAACCTAGT			931
292	A A W A V A R A T L A D A R C W E L S A			311
	1030	1050	1070	
932	CTGGAGACATCAAGTGGATTATCAAGCACCGATCTAGCAGCTATTGGGCTGAATTITA			991
312	G D I K W I Y Q A P I L A A I G L N F I			331
	1090	1110	1130	
992	TTCTGTTCTGAATAACGGTTAGAGTTCTAGCTACAAAATCTGGAGACCAATGCAGTTG			1051
332	L F L N T V R V L A T K I W E T N A V G			351
	1150	1170	1190	
1052	GGCATGACACAAGGAAGCAATAACAGGAAACTGCCAACATGACACTGGCCTGGTCCTAG			1111
352	H D T R K Q Y R K L A K S T L V L V L V			371
	1210	1230	1250	
1112	TCTTGAGTGCATTACATCGTGTGCTGCCTCACTCCTTCACTGGGCTCGGGT			1171
372	F G V H Y I V F V C L P H S F T G L G W			391
	1270	1290	1310	
1172	GGGAGATECGCATGCACTGTGAGCTTCTTCAACTCCTTCAGGGTTCTTGTGTCTA			1231
392	E I R M H C E L F F N S F Q G F F V S I			411
	1330	1350	1370	
1232	TCATCTACTGCTACTGCAATGGAGAGGTTCAAGCAGAGGTGAAGAAGATGTGGAGTCGGT			1291
412	I Y C Y C N G E V Q A E V K K M W S R W			431
	1390	1410	1430	
1292	GGAATCTCTCGTGGACTGGAAAAGGACACCGCCATGTGGCAGCCGCAGATGCAGCTAG			1351
432	N L S V D W K R T P P C G S R R C G S V			451
	1450	1470	1490	
1352	TGCTCACCAACCGTGACGCACAGCACAGCAGCCAGTCACAGGTGGCGAGCACACGCAT			1411
452	L T T V T H S T S S Q S Q V A A A H A W			471
	1510	1530	1550	

FIGURE 1 2/3

1412 GGTGCTTATCTCTGGCAAAGCTGCCAAGATGCCAGCAGACAGCCTGACAGCCACATCAC 1471
472 C L S L A K L P R S P A D S L T A T S L 491

1570 1590 1610
1472 TTTACCTGGCTATGTCTGGAGTAACTCAGAGCAGGACTGCCTCACACACTCTCCACGA 1531
492 Y L A M S G V T Q S R T A S H T L S T R 511

1630 1650 1670
1532 GGAGCAACAAGGAAGATAGTGGGAGGCAGAGAGATGATATTCTAATGGAGAAGCCTCCA 1591
512 S N K E D S G R Q R D D I L M E K P S R 531

1690 1710 1730
1592 GGCCTATGGAATCTAACCCAGACACTGAAGGATGACAAGGAGAAACTGAGGATGTTCTCT 1651
532 P M E S N P D T E G 541

1750 1770 1790
1652 GAATGGACATGTGTGGCTGACTTTCATGGGCTGGCCAATGGCTGGTGTGAGAGGGC 1711

1810 1830 1850
1712 TTGGCTGATACTCTATGCTTGAGCACAAAGGCTGAAAATTCAAGTTAAGGTGTTACTAA 1771

1870 1890 1910
1772 TAATAGTTTTAGGCTCCATGAATTGGCTCTGTAAACTAACGACATGAAAATGCAAG 1831

1930 1950 1970
1832 TGTCAATGGAGTAGTTATTACCTCTATTGGCATCAAGTTCTCTAAATTATGTAT 1891

1990
1892 GGTATTTGCTCTGTGATTGTTCA 1914

FIGURE 1 3/2

Friday, May 5, 1995 11:45 AM

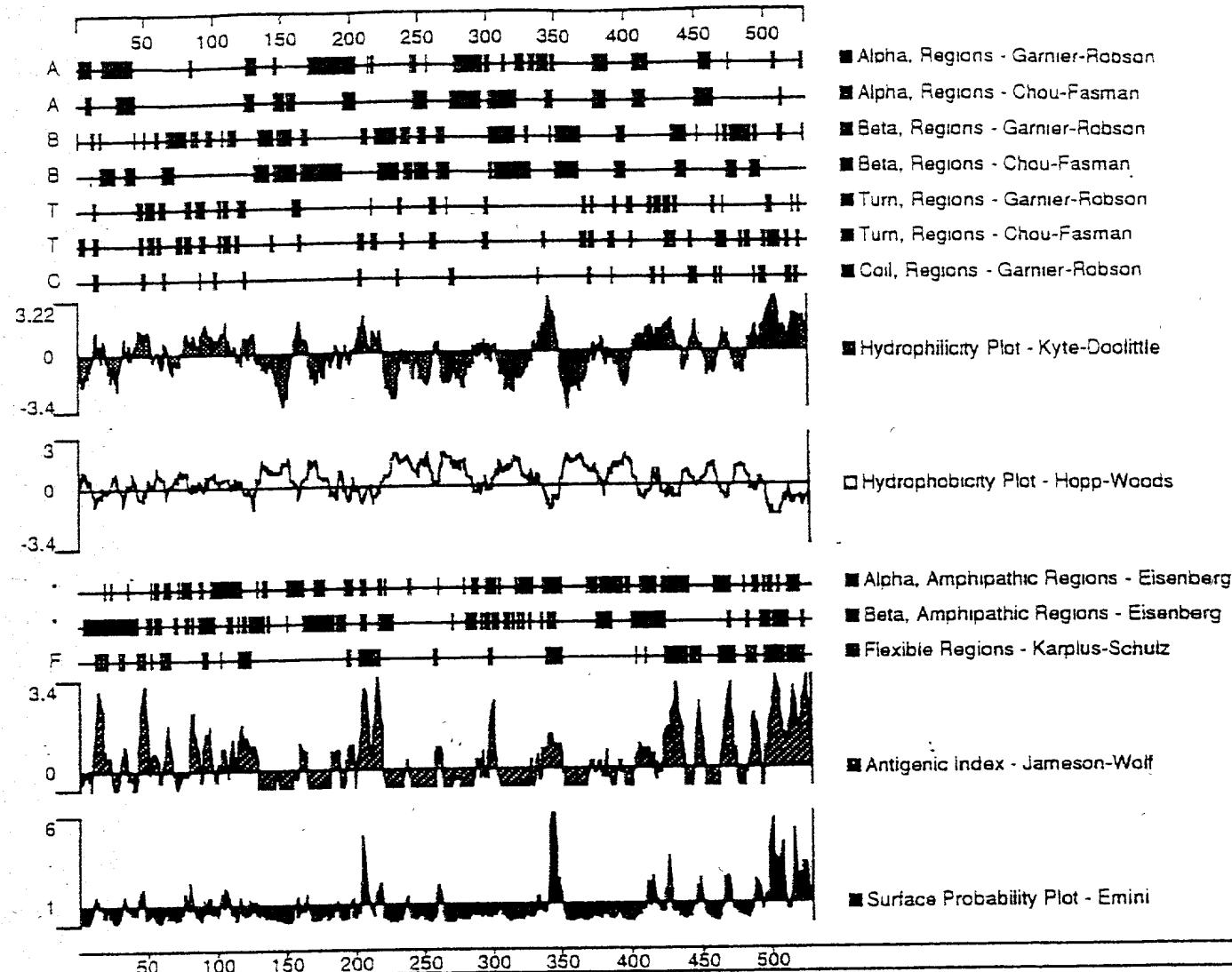


FIGURE 2 111

Sequences producing High-scoring Segment Pairs: Fr. Score P(N) ::

gp M74445 OPOPTHR_1	parathyroid hormone receptor [Didelphis virginiana]	+3	597	8.2e-204	6
pir SIA39286	parathyroid hormone / parathyroid hormone receptor	+3	597	8.2e-204	6
gp L04308 HUMPTHR_1	parathyroid hormone receptor [Homo sapiens]	+3	580	6.7e-190	5
pir SIS29610	parathyroid hormone receptor - human	+3	580	6.1e-189	5
gp M77184 RATPATHYR_1	parathyroid hormone receptor [Rattus norvegicus]	+3	576	7.7e-188	5
gp X78936 MMMPHRPR_1	parathyroid hormone/parathyroid hormone receptor	+3	576	7.7e-188	5
pir SIA42698	parathyroid hormone and parathyroid hormone receptor	+3	576	7.7e-188	5
gp L34611 MUSPTHR06_1	parathyroid hormone/parathyroid hormone receptor	+3	576	4.1e-174	5
gp U11087 HSV1RG9_1	vasoactive intestinal peptide 1	+3	319	1.2e-98	5
gp M86835 RATVASREC_1	vasoactive intestinal polypeptide receptor	+3	254	3.1e-91	5

WARNING: Descriptions of 49 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|M74445|OPOPTHR_1 parathyroid hormone receptor [Didelphis virginiana]
Length = 585

Plus Strand HSPs:

Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Query: 729 IMQDDPQNSIEATSVDKSQYIGCKIAVMFIYFLATNYYWILVEGLYLHNLI[F]AFFSDT 908
I +++ + E DK+ ++GC++AV +F+YFL TNYYWILVEGLYLH+LIF+AFFS+
Sbjct: 253 ITEEELRAFTEPPPAGKAGFVGCRVAVTVFLYFLTTNYYWILVEGLYLHSLIFMAFFSEK 312

Query: 909 KYLGWFGILINGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLN[F]ILF 1088
KYLWGFLGWG PA FVA W RATLA+ CW+LS+G+ KWI Q PILAAI +NFILF
Sbjct: 313 KYLGWFTLFGWGLPAVFVAVWVTVRATLANECWDLSSGNKKWIIQVPILAAIVVN[F]ILF 372

Query: 1089 LNTVRVLATKIKWETNAVGHDTRKQYRKAKSTLVLVLFVGVHYIVFVCLPHS 1244
+N +RVLATK+ ETNA DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++
Sbjct: 373 INIIRVLATKLRRETNAGRCDTRQQYRKLLKSTLVLMLPLFGVHYIVFMATPYT 424

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

Query: 267 EGNCFPEWDGLICWPRGTVGKISAVPCPP[Y]IYDFNHKGVAFRHCNPNGTWDFMHSINKTW 446
+G C PEWD ++CWP G GK+ AVPCP YIYDFNHKG A+R C+ NG+W+ + N+TW
Sbjct: 102 DGFC[LP]EWDTIVCWPAGVPGKVVAVPCPDYIYDFNHKG[RAYRRCDSNGSWELVPGNNRTW 161

Query: 447 ANYSDCLRFL 476
ANYSDCLRFL
Sbjct: 162 ANYSECVKFL 171

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

Query: 498 KQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRNYIHMHLFVFSMLRATSIFV 677
++E +RL ++YTVGYSIS GSL VA+LI+GYFRLHCTRNYIHMHLFVFSMLRA SIF+
Sbjct: 177 EREVFDRLGMIYT[TVGYSISLGSLTAVLILGYFRLHCTRNYIHMHLFVFSMLRAVSIFI 236

Query: 678 KDRVVAHIGVKELESIMQD 740
KD V+++ + E+E + ++
Sbjct: 237 KDAVLVSGVSTD[EIERITEEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query: 1248 TGLGWEIRMHCELFNSPQGFFVSI[IYCYCN]GEVQAEVKKMWSRWNLSDWKRTPPCGS 1424

FIGURE 3

-G+ W++M + FNSFQGFFFV+IIYC+CNGEVQAE+KK' WS L++D+KG GS
Sbjct: 427 SGILWQVQMHxLMLFNSFQGFFVALIYCFNNGEVQAEIKKSWS LALDFKRKARSGS 425

Score = 72 (33.1 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query: 159 AQLDSDGTTITIEEQIVLVVLKAKVQCELNITAQLQEGER 269

A +D+D IT EEQI+L+ A+ QCE + L+ E

Sbjct: 24 ALVDADDVITKEEQIILLRNAQAQCEQRALKEVLRVPE 60

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query: 1508 ISGKAAKIASRQPDSHITLPGYV 1576

+S + A A + H LPGYV

Sbjct: 512 LSPRLAPGAGASANGHHQLPGYV 534

FIGURE 3